

result	No.	Score	Query	Match	Length	DB	ID	Description
1	209	67.4	Q9BX67	310	4	Q9BX67		Q9bx67 homo sapien
2	209	67.4	Q8WWL8	355	4	Q8WWL8		Q8wwl8 homo sapien
3	134	43.2	Q96FL1	309	4	Q96FL1		Q96fl1 homo sapien
4	32	10.3	Q9DBB7	310	1	Q9DBB7		Q9dbb7 mus musculu
5	28	9.0	Q9D1M9	310	11	Q9D1M9		Q9d1m9 mus musculu
6	28	9.0	Q9EPK4	310	11	Q9EPK4		Q9epk4 mus musculu
7	13	4.2	Q8BT59	64	11	Q8BT59		Q8bt59 mus musculu
8	8	2.6	Q9TNT2	39	7	Q9TNT2		Q9tnT2 homo sapien
9	8	2.6	Q8HWG1	67	7	Q8HWG1		Q8hwg1 homo sapien
10	8	2.6	Q818S1	131	5	Q818S1		Q818s1 anopheles g
11	8	2.6	Q8CAV2	154	11	Q8CAV2		Q8caV2 mus musculu
12	8	2.6	Q8TQ15	231	17	Q8TQ15		Q8tq15 methanosaarc
13	8	2.6	Q8ZSR8	232	17	Q8ZSR8		Q8zsR8 pyrobaculum
14	8	2.6	Q91R49	233	10	Q91R49		Q91r49 arabidopsis
15	8	2.6	Q966CO	246	7	Q966CO		Q966cO mus musculu
16	8	2.6	Q966CO	290	7	Q966CO		Q966cO mus musculu

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query			DB	ID	Description
		Match	Length	ID			
1	209	67.4	310	4	Q9BX67	homo sapien	Q9bx67
2	209	67.4	355	4	Q8WNL8	homo sapien	Q8wnl8
3	134	63.2	309	4	Q96FL1	homo sapien	Q96fl1
4	32	10.3	310	11	Q9DB77	mus musculus	Q9db77
5	28	9.0	310	11	Q9DM9	mus musculus	Q9dm9
6	28	9.0	310	11	Q9PK4	mus musculus	Q9pk4
7	13	4.2	64	11	Q8BT59	mus musculus	Q8bt59
8	8	2.6	39	7	Q9TNT2	homo sapien	Q9tnnt2
9	8	2.6	67	7	Q8HMG1	homo sapien	Q8hmg1
10	8	2.6	131	5	Q8IBS1	anopheles g	Q8ibs1
11	8	2.6	154	11	Q8CV2	mus musculus	Q8cv2
12	8	2.6	231	17	Q8IQF5	methanobacter	Q8iqf5
13	8	2.6	232	17	Q8ZRR8	pyrobaculum	Q8zrr8
14	8	2.6	233	10	Q9LR49	arabidopsis	Q9lr49
15	8	2.6	246	5	Q966C0	caenorhabdi	Q966c0
16	8	2.6	290	7	Q29990	homosancti	Q29990



Qy	1	MALRRPPRLCARLPDFLLLFRGCLIGAVNLKSSNRTPVQFESVELSCLITDQT	60		PRELIMINARY;	PRT;	310 AA.
Db	46	MAIRRPPRLCARLPDFLLLFRGCLIGAVNLKSSNRTPVQFESVELSCLITDQT	105	17	Created)		
Db	61	SDPRIEWKIQDEQTTYFFDNKIQGDLGRAEILGKTSKLNNTTRDSALYRCEVVAR	120	17	Last sequence update)		
Qy	106	SDPRIEWKIQDEQTTYFFDNKIQGDLGRAEILGKTSKLNNTTRDSALYRCEVVAR	165	23	Last annotation update)		
Db		Mus musculus (Mouse)					
Qy	121	NDKEIDIEVIEITVQVTPVTPCRVPKAVPVGKMATLHQSESEGHRPHYSWYRNDPL	180	OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Db	166	NDKEIDIEVIEITVQVTPVTPCRVPKAVPVGKMATLHQSESEGHRPHYSWYRNDPL	225	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
Db		NCBI_TaxID=10500;		OC			
Qy	181	PTDSRANPRFNSHINSETGTIVPVAHKDSDGQYCTIASNDGARCEQEMEVYDL	240	RN	SEQUENCE FROM N.A.		
Db	226	PTDSRANPRFNSHINSETGTIVPVAHKDSDGQYCTIASNDGARCEQEMEVYDL	285	RX	STRAIN=C57BL/6J; TISSUE=Small intestine;		
Qy	241	NIGGIIGGVLYVLAIVLTLGICCAYRGYFINKQDGESYKNPGKDPGVNIRTEDEG	300	RA	MEDLINE=21085660; PubMed=11217851;		
Db	286	NIGGIIGGVLYVLAIVLTLGICCAYRGYFINKQDGESYKNPGKDPGVNIRTEDEG	345	RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
Qy	301	DPEHKSSSVI 310		RA	Arai K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
Db	346	DPEHKSSSVI 355		RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakawa I.,		
Db				RA	Saito T., Okazaki Y., Gejohori T., Bono H., Kasukawa T., Saito R.,		
Db				RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
Db				RA	Fleischmann W., Gaasterland T., Glesis C., King B., Kochiba H.,		
Qy	301	DPEHKSSSVI 310		RA	Kuehl P., Lewis S., Matsuo Y., Niitaido I., Pesole G., Quackenbush J.,		
Db	346	DPEHKSSSVI 355		RA	Schramm L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,		
Db				RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
Db				RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,		
Db				RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
Db				RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,		
Db				RA	Lyons P., Marchionni L., Mashima J., Marzarella J., Mombaerts P.,		
Db				RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
Db				RA	Sasaki H., Sato K., Schoenbach C., Seya T., Storch K.-F.,		
Db				RA	Suzuki H., Toyoo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,		
Db				RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,		
Db				RA	Hayashizaki Y.;		
Db				RT	"Functional annotation of a full-length mouse cDNA collection."		
Db				RL	Nature 409:685-690 (2001)		
Db				DR	EMBL; AK008187; BAB25519..1..;		
Db				DR	MGI; MGI:19333820; Jcam2..1..;		
Db				DR	MGD; MGI:19333825; Jcam3..1..;		
Db				DR	Intertiro; IPR007110; Ig-like.		
Db				DR	Intertiro; IPR003598; Ig_c2..		
Db				DR	Intertiro; IPR003006; Ig_MHC.		
Db				DR	PF00047; 19..2..;		
Db				DR	SMART; SM00408; IgC2..1..		
Db				DR	PROSITE; PS50835; Ig_LIKE..2..		
Db				KW	Immunoglobulin domain.		
Db				SQ	SEQUENCE 310 AA; 34855 MW; C74384EAB234680 CRC64;		
Db				Query	Match Score 10..3%; Best Local Similarity 100.0%; Matches 32;		
Db				Match	DB 11; Length 310; Pred. No. 6..8e-25; Conservative 0;		
Db				Match	Mismatches 0; Indels 0; Gaps 0;		
Db				Qy	41 PVVQEFEVSLCITDQSQTSDPRTEWKID 72		
Db				Db	41 PVVQEFEVSLCITDQSQTSDPRTEWKID 72		
Db				RESULT 5			
Db				Q9D1M9			
Db				AC	Q9D1M9 PRELIMINARY;	PRT;	310 AA.
Db				DT	01-JUN-2001 (TREMBLrel. 17, Created)		
Db				DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
Db				DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
Db				DE	1110002N23Rik protein.		
Db				GN	JCAM3 OR JCAM2 OR 1110002N23RIK.		
Db				OS	Mus musculus (Mouse)		
Db				OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
Db				OC	NCBI_TaxID=10900;		
Db				RN	SEQUENCE FROM N.A.		
Db				RP	STRAIN=C57BL/6J; TISSUE=Embryo;		
Db				RC	MEDLINE=21085660; PubMed=11217851;		
Db				RX			
Qy	2	ALRRPPRLCARLPDFLLLFRGCLIGAVNLKSSNRTPVQFESVELSCLITDQS	61				
Db	1	ALRRPPRLCARLPDFLLLFRGCLIGAVNLKSSNRTPVQFESVELSCLITDQS	60				
Qy	62	DPLIEWKIQDEQTTYFFDNKIQGDLGRAEILGKTSKLNNTTRDSALYRCEVVAR	121				
Db	61	DPLIEWKIQDEQTTYFFDNKIQGDLGRAEILGKTSKLNNTTRDSALYRCEVVAR	120				
Qy	122	DRKEIDIEVIEITVQVTPVTPCRVPKAVPVGKMATLHQSESEGHRPHYSWYRNDPL	135				
Db	121	DRKEIDIEVIEITVQVTPVTPCRVPKAVPVGKMATLHQSESEGHRPHYSWYRNDPL	134				
Qy	123	DRKEIDIEVIEITVQVTPVTPCRVPKAVPVGKMATLHQSESEGHRPHYSWYRNDPL	134				
Qy	124	DRKEIDIEVIEITVQVTPVTPCRVPKAVPVGKMATLHQSESEGHRPHYSWYRNDPL	134				

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 Arakawa T., Hara A., Fukunishi H., Konno H., Adachi J., Fukunaka S.,  
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 Saito T., Okazaki Y., Gojobori T., Bono H., Kubukawa T., Saito R.,  
 Kadota K., Matsuda H.A., Asburner M., Battalov S., Casavant T.,  
 Pleischmann W., Gasterland T., Gissi S., King B., Kochiwa H.,  
 Kushi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 Blake J., Bottefoglio D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 Brownstein M.J., Built C., Fletcher C., Fujita M., Garibaldi M.,  
 Gustincovich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 Sasada H., Sato K., Schoenbach C., Seiya T., Shibata Y., Storch K.-F.,  
 Suruki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 Wynnshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,  
 Hayashizaki Y., RTRT  
 "Functional annotation of a full-length mouse cDNA collection.";  
 Nature 409: 685-690 (2001).  
 ENSEMBL: AK003326; BAB22715.1; -.  
 MGD: MGJ:1933820; Jcam3.  
 MGD: MGJ:1933825; Jcam3.  
 InterPro: IPR007110; Ig-like.  
 InterPro: IPR003598; Ig\_C2.  
 InterPro: IPR003006; Ig\_MHC.  
 SMART: SM00408; IgC2\_1.  
 PROSITE: PS50035; Ig\_LIKE\_2.  
 Immunoglobulin domain.  
 SEQUENCE: 310 AA; 3419 MW; 6628BCAD68E44B1D CRC64;

RESULT 6						
	Q9FPK4	Q9FPK4	PRELIMINARY;	PRT;	310 AA.	
Qy	45. EFEESVELSCILITDQSQTSDPRIEWKKIQQ 72					
Db		45 EFEESVELSCILITDQSQTSDPRIEWKKIQQ 72				
Query Match	9.0%	Score 28;	DB 11;	Length 310;		
Best Local Similarity	100.0%	Pred. No. 1.e-20;				
Matches	28;	Conservative	0;	Mismatches	0;	Gaps 0;
Indels						

SPBAIN-057BL/6J; TISSUE-Embryo;  
MEDLINE-21085660; PubMed-1217851;  
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
Aizawa K., Iwasa M., Nishi K., Kiyoasa H., Kondo S., Yamana I.,  
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
Pleischmann W., Gaasterland T., Gissi C., King B., Kohwi H.,  
Kuehl P., Lewis S., Matsuo Y., Nikaiko C., Pesole G., Quackenbush J.,



Q8TQ5	OBTQ5	PRELIMINARY;	PRT;	231 AA.	QY	17 DFFFLLF 24               2 DFFFLLF 9
ID	Q8TQ5;				Db	
AC	Q8TQ5;				Q9LR49	PRELIMINARY;
DT	01-JUN-2002	(TREMBLrel. 21, Created)			AC	Q9LR49;
DT	01-JUN-2002	(TREMBLrel. 21, Last sequence update)			DT	01-OCT-2000 (TREMBLrel. 15, Created)
DE	Cell surface lipoprotein.				DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
MA1454.					DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)
OS	Methanoscirrhus acetivorans.				DE	T25H20.10.
OC	Archaea; Buryarchaeota; Methanococci; Methanoscirrales;				OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Methanococcaceae; Methanoscirrata.				OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
NCBI_TaxID	2214;				OC	Spematophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
RN					OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.
RP	SEQUENCE FROM N.A.				RA	SEQUENCE FROM N.A.
RC	STRAIN=C2A / ATCC 35395 / DSM 2834;				RA	Johnson-Hopson C., Brooks S., Buehler E., Chao Q., Khan S., Kim C.,
RX	MEDLINE=21929760; PubMed=1193238;				RA	Shinn P., Altaf H., Bei Q., Chin C., Chiu J., Choi E., Conn L.,
RA	Galzane J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,				RA	Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA	FitzHigh W., Calvo S., Engels R., Smirnov S., Attnor D., Brown A.,				RA	Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA	Allen N., Naylor J., Strange-Thomann N., Dearallano K., Johnson R.,				RA	Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA	Linton L., McEvans P., McIernan K., Talana J., Turrell A., Ye W.,				RA	Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA	Zimmer A., Barber R.D., Cann J., Graham D.E., Grahame D.A., Guss A.M.,				RA	Ecker J.R.;
RA	Hedderich R., Ingram-Smith C., Kuettertner H.C., Kryczki J.A.,				RT	"Genomic sequence for Arabidopsis thaliana BAC T25N20 from chromosome
RA	Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,				RT	I."
RA	Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,				RT	Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RA	Perry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,				RT	
RA	Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,				RT	
RA	Metcalf W.W., Birren B.,				RL	
RT	"The genome of Methanoscirratus acetivorans reveals extensive metabolic				RL	
RT	and physiologically diversity";				RL	
RT	Genome Res. 12:532-542 (2002);				RL	
DR	EMBL; AB010815; AAM04868.1; -.				RA	Ecker J.R.;
KW	Lipoprotein; Complete proteome;				RA	SEQUENCE FROM N.A.
SEQUENCE	231 AA; 25437 MW; 7AA21CCE0B6500B CRC64;				RL	Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
SO					RA	
Query Match	2.6%; Score 8; DB 17; Length 231;				RA	
Best Local Similarity	100.0%; Pred. No. 11;				RA	
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				RA	
QY	250 LVVLAVIA 257				RA	
Db	23 LVVLAVIA 30				RA	
RESULT 13					RA	
Q8ZSR8	Q8ZSR8	PRELIMINARY;	PRT;	232 AA.	RA	
ID	Q8ZSR8;				RA	
AC	Q8ZSR8;				RA	
DT	01-MAR-2002	(TREMBLrel. 20, Created)			RA	
DT	01-MAR-2002	(TREMBLrel. 20, Last sequence update)			RA	
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)			RA	
DE	Hypothetical protein PAE614.				RA	
GN	PAE614.				RA	
OS	Pyrococcus aerophilum.				RA	
OC	Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;				RA	
OC	Thermoproteaceae; Pyrococcus.				RA	
NCBI_TaxID	13773;				RA	
RN					RA	
RP	SEQUENCE FROM N.A.				RA	
RC	STRAIN=C2A / ATCC 51768 / DSM 7523;				RA	
RX	PubMed=11792869;				RA	
RA	Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,				RA	
RA	Miller J.H.;				RA	
RT	"Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum";				RA	
RT	Proc. Natl. Acad. Sci. U.S.A. 99:984-989 (2002).				RA	
DR	EMBL; AE009941; AAL65045.1; -.				RA	
KW	Hypothetical protein; Complete proteome.				RA	
SEQUENCE	232 AA; 25942 MW; 39ASBCC4403F903 CRC64;				RA	
SO					RA	
Query Match	2.6%; Score 8; DB 17; Length 232;				DR	
Best Local Similarity	100.0%; Pred. No. 11;				DR	
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				DR	
QY	2.6%; Score 8; DB 10; Length 233;				DR	
Db	233 AA; 24829 MW; 28AD613BB085D58D CRC64;				DR	
Query Match	2.6%; Score 8; DB 10; Length 233;				DR	

Best Local Similarity 100.0% ; Pred. No. 11 ; Mismatches 0 ; Indels 0 ; Gaps 0	
Qy	56 TDSQTSDP 63
Db	122 TDSQTSDP 129
RESULT 15	
Q96650	PRELIMINARY ; PRT ; 246 AA.
ID Q96650	
AC Q96650;	
DT 01-DEC-2001 (TREMBLrel. 19, Created)	
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	
DB Hypothetical protein Y45G12B.2b.	
GN Y45G12B.2.	
OS Caenorhabditis elegans.	
OC Buletaria; Metzolia; Nematoda; Chromadorea; Rhabditoidea; Rhabditidae; Peledoxinae; Caenorhabditis.	
OC NCBI_TaxID=6239;	
RN [1]	SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;	
RC RX MEDLINE=90069613; PubMed=9851916;	
RA None;	
RT "Genome sequence of the nematode <i>C. elegans</i> : a platform for investigating biology. The <i>C. elegans</i> Sequencing Consortium." [2]	
RN [2]	SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;	
RC Bradshaw H., Graves T., Fronick B. ; RA Waterston R. ; RT "The sequence of the <i>C. elegans</i> coomid Y45G12B." ; RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	
RN [3]	SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;	
RC RA Waterston R. ; RT "Direct Submission." ; RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.	
DR EMBL; ACO06768; AAC070665.1; -.	
DR Wormpep; Y45G12B.2b; CE2B365;	
SQ SEQUENCE 246 AA; 27463 MW; CBEF536A113A2050 CRC64;	
Query Match Score 8 ; DB 5 ; Length 246;	
Best Local Similarity 100.0% ; Pred. No. 11 ; Mismatches 0 ; Indels 0 ; Gaps 0	
Qy	253 LAVLALIT 260
Db	199 LAVLALIT 206
RESULT 16	
Q29990	PRELIMINARY ; PRT ; 290 AA.
ID Q29990	
AC Q29990;	
DT 01-NOV-1996 (TREMBLrel. 01, Created)	
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	
DE MHC class I lymphocyte antigen (Fragment).	
GN Homo sapiens (Human).	
OC Eukaryota; Metzolia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.	
OC NCBI_TaxID=9606;	
RN [1]	SEQUENCE FROM N.A.
RP MEDLINE=8233329; PubMed=2714852;	
RC Pohla H., Kuoh W., Tabaczewski P., Doerner C., Weiss E.H. ; RA "Allelic variation in HLA-B and HLA-C sequences of the HLA-B alleles." ; RT	

RESULT 18							
Q9N4Y9	PRELIMINARY;	PRT;	309 AA.				
ID	Q9N4Y9						
AC	Q9N4Y9						
DT	01-OCT-2000 (TREMBLrel: 15; Created)						
DR	AP001003; BAB50858; -						
KW	Hypothetical protein; Complete proteome						
SQ	294 AA; 30575 MW; C17AB5E56B64A5A6 CRC64;						
RESULT 17							
Q98EQ9	PRELIMINARY;	PRT;	294 AA.				
ID	Q98EQ9						
AC	Q98EQ9						
DT	01-OCT-2001 (TREMBLrel: 18; Created)						
DT	01-OCT-2001 (TREMBLrel: 18; Last sequence update)						
DT	01-OCT-2002 (TREMBLrel: 22; Last annotation update)						
DE	Hypothetical protein m114127.						
GN	M114127.						
OS	Rhizobium loti (Mesorhizobium loti).						
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;						
OC	Phyllobacteriaceae; Mesorhizobium.						
OC	NCBI_TaxID381;						
RN	SEQUENCE FROM N.A.						
RC	STRAIN=MAF3030309; PubMed=11214968;						
RX	SEQUENCE FROM N.A.						
RA	Medline=21082930; Pubmed=11214968;						
RA	Kato T., Sasamoto S., Kato T., Sasamoto S.,						
RA	Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,						
RA	Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,						
RA	Mochizuki Y., Nakayama S., Nakazaki N., Shimpou S., Sugimoto M.,						
RA	Takeuchi C., Yamada M., Tabata S.;						
RT	"Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti."						
RT	DNA Res. 7:331-338 (2000).						
DR	7:331-338 (2000).						
KW							
HYPOTHETICAL							
SQ	294 AA; 30575 MW; C17AB5E56B64A5A6 CRC64;						
RESULT 16							
Q98EQ9	PRELIMINARY;	PRT;	294 AA.				
ID	Q98EQ9						
AC	Q98EQ9						
DT	01-OCT-2000 (TREMBLrel: 15; Created)						
DR	AP001003; BAB50858; -						
KW	Hypothetical protein; Complete proteome						
SQ	294 AA; 30575 MW; C17AB5E56B64A5A6 CRC64;						
RESULT 15							
Q98EQ9	PRELIMINARY;	PRT;	294 AA.				
ID	Q98EQ9						
AC	Q98EQ9						
DT	01-OCT-2000 (TREMBLrel: 15; Created)						
DR	AP001003; BAB50858; -						
KW	Hypothetical protein; Complete proteome						
SQ	294 AA; 30575 MW; C17AB5E56B64A5A6 CRC64;						
RESULT 14							
Q98EQ9	PRELIMINARY;	PRT;	294 AA.				
ID	Q98EQ9						
AC	Q98EQ9						
DT	01-OCT-2000 (TREMBLrel: 15; Created)						
DR	AP001003; BAB50858; -						
KW	Hypothetical protein; Complete proteome						
SQ	294 AA; 30575 MW; C17AB5E56B64A5A6 CRC64;						
RESULT 13							
Q98EQ9	PRELIMINARY;	PRT;	294 AA.				
ID	Q98EQ9						
AC	Q98EQ9						
DT	01-OCT-2000 (TREMBLrel: 15; Created)						
DR	AP001003; BAB50858; -						
KW	Hypothetical protein; Complete proteome						
SQ	294 AA; 30575 MW; C17AB5E56B64A5A6 CRC64;						
RESULT 12							
Q98EQ9	PRELIMINARY;	PRT;	294 AA.				
ID	Q98EQ9						
AC	Q98EQ9						
DT	01-OCT-2000 (TREMBLrel: 15; Created)						
DR	AP001003; BAB50858; -						
KW	Hypothetical protein; Complete proteome						
SQ	294 AA; 30575 MW; C17AB5E56B64A5A6 CRC64;						
RESULT 11							
Q98EQ9	PRELIMINARY;	PRT;	294 AA.				
ID	Q98EQ9						
AC	Q98EQ9						
DT	01-OCT-2000 (TREMBLrel: 15; Created)						
DR	AP001003; BAB50858; -						
KW	Hypothetical protein; Complete proteome						
SQ	294 AA; 30575 MW; C17AB5E56B64A5A6 CRC64;						
RESULT 10							
Q98EQ9	PRELIMINARY;	PRT;	294 AA.				
ID	Q98EQ9						
AC	Q98EQ9						
DT	01-OCT-2000 (TREMBLrel: 15; Created)						
DR	AP001003; BAB50858; -						
KW	Hypothetical protein; Complete proteome						
SQ	294 AA; 30575 MW; C17AB5E56B64A5A6 CRC64;						
RESULT 9							
Q98EQ9	PRELIMINARY;	PRT;	294 AA.				
ID	Q98EQ9						
AC	Q98EQ9						
DT	01-OCT-2000 (TREMBLrel: 15; Created)						
DR	AP001003; BAB50858; -						
KW	Hypothetical protein; Complete proteome						
SQ	294 AA; 30575 MW; C17AB5E56B64A5A6 CRC64;						
RESULT 8							
Q98EQ9	PRELIMINARY;	PRT;	294 AA.				
ID	Q98EQ9						
AC	Q98EQ9						
DT	01-OCT-2000 (TREMBLrel: 15; Created)						
DR	AP001003; BAB50858; -						
KW	Hypothetical protein; Complete proteome						
SQ	294 AA; 30575 MW; C17AB5E56B64A5A6 CRC64;						
RESULT 7							
Q98EQ9	PRELIMINARY;	PRT;	294 AA.				
ID	Q98EQ9						
AC	Q98EQ9						
DT	01-OCT-2000 (TREMBLrel: 15; Created)						
DR	AP001003; BAB50858; -						
KW	Hypothetical protein; Complete proteome						
SQ	294 AA; 30575 MW; C17AB5E56B64A5A6 CRC64;						
RESULT 6							
Q98EQ9	PRELIMINARY;	PRT;	294 AA.				
ID	Q98EQ9						
AC	Q98EQ9						
DT	01-OCT-2000 (TREMBLrel: 15; Created)						
DR	AP001003; BAB50858; -						
KW	Hypothetical protein; Complete proteome						
SQ	294 AA; 30575 MW; C17AB5E56B64A5A6 CRC64;						
RESULT 5							
Q98EQ9	PRELIMINARY;	PRT;	294 AA.				
ID	Q98EQ9						
AC	Q98EQ9						
DT	01-OCT-2000 (TREMBLrel: 15; Created)						
DR	AP001003; BAB50858; -						
KW	Hypothetical protein; Complete proteome						
SQ	294 AA; 30575 MW; C17AB5E56B64A5A6 CRC64;						
RESULT 4							
Q98EQ9	PRELIMINARY;	PRT;	294 AA.				
ID	Q98EQ9						
AC	Q98EQ9						
DT	01-OCT-2000 (TREMBLrel: 15; Created)						
DR	AP001003; BAB50858; -						
KW	Hypothetical protein; Complete proteome						
SQ	294 AA; 30575 MW; C17AB5E56B64A5A6 CRC64;						
RESULT 3							
Q98EQ9	PRELIMINARY;	PRT;	294 AA.				
ID	Q98EQ9						
AC	Q98EQ9						
DT	01-OCT-2000 (TREMBLrel: 15; Created)						
DR	AP001003; BAB50858; -						
KW	Hypothetical protein; Complete proteome						
SQ	294 AA; 30575 MW; C17AB5E56B64A5A6 CRC64;						
RESULT 2							
Q98EQ9	PRELIMINARY;	PRT;	294 AA.				
ID	Q98EQ9						
AC	Q98EQ9						
DT	01-OCT-2000 (TREMBLrel: 15; Created)						
DR	AP001003; BAB50858; -						
KW	Hypothetical protein; Complete proteome						
SQ	294 AA; 30575 MW; C17AB5E56B64A5A6 CRC64;						
RESULT 1							
Q98EQ9	PRELIMINARY;	PRT;	294 AA.				
ID	Q98EQ9						
AC	Q98EQ9						
DT	01-OCT-2000 (TREMBLrel: 15; Created)						
DR	AP001003; BAB50858; -						
KW	Hypothetical protein; Complete proteome						
SQ	294 AA; 30575 MW; C17AB5E56B64A5A6 CRC64;						

DT 01-OCT-2000 (TREMBLrel. 15; Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)  
 DR Hypothetical 34.8 kDa protein.  
 GN Y45G12B.2.  
 OC Caenorhabditis elegans.  
 Eukaryota; Metazoa; Nematoidea; Rhabditida; Rhabditidae; Peledorinae; Caenorhabditis.  
 OC NCBI TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 STRAIN=Bristol N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA None;  
 RA "Genome sequence of the nematode *C. elegans*: a platform for investigating biology. The *C. elegans* Sequencing Consortium.";  
 Science 289;2012-2018 (1998).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC Bradshaw H., Graves T., Fronick B.;  
 RA "The sequence of *C. elegans* cosmid Y45G12B.;"  
 RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Waterston R.;  
 RT "Direct Submission."  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC006168; AAF60574.1;  
 DR WormPep; Y45G12B.2a; CE21934;  
 DR InterPro; IPR001841; Znf\_ring.  
 DR SMART; SM00184; RING\_1.  
 DR PROSTREB; PS50089; ZF\_RING\_2; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 309 AA; 34815 MW; CF6D5930D192D CRC64;  
 Query Match 2.6%; Score 8; DB 5; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DR 253 LAVLALIT 260  
 Db 262 LAVLALIT 269

RESULT 19  
 Q9MY31 PRELIMINARY; PRT; 313 AA.  
 ID Q9MY31; PRELIMINARY; PRT; 313 AA.  
 AC 09MY31; PRELIMINARY; PRT; 313 AA.  
 DT 01-OCT-2000 (TREMBLrel. 15; Created)  
 DT 01-OCT-2000 (TREMBLrel. 15; Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)  
 DE Human leucocyte antigen C (Fragment).  
 GN Homo sapiens (Human).  
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC NCBI TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99116847; PubMed=10488744;  
 RA van der Vlies S.A., Voorter C.B., van den Berg-Loonen E.M.;  
 RT "There is more to HLA -C than exons 2 and 3: sequencing exons 1, 4 and 5."  
 RT Tissue Antigens 54:169-177 (1999).  
 CC -; FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).  
 CC -; SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).  
 CC EMBL; Y18533; CAB71800.1;  
 DR EMBL; Y18534; CAB71800.1; JOINED.  
 DR EMBL; Y18535; CAB71800.1; JOINED.  
 DR EMBL; Y18536; CAB71800.1; JOINED.

DR HSSP; P30685; 1A9E.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_C1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR001039; MHC\_1.  
 DR Pfam; PF00047; Ig\_1.  
 DR Pfam; PF00129; MHC\_1.  
 DR PRINTS; PRO1638; MHCCLASS1.  
 DR ProDom; PD000050; MHC\_1.  
 DR SMART; SM04007; IgC1\_1.  
 DR PROSITE; PS50335; Ig\_Like; 1.  
 KW Glycoprotein; Transmembrane.  
 FT NON-TER 1  
 SQ SEQUENCE 313 AA; 313 MW; 2BFD5D879ECCF238F CRC64;  
 Query Match 2.6%; Score 8; DB 7; Length 313;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DR 249 VLVVLAVL 256  
 Db 292 VLVVLAVL 299

RESULT 20  
 Q9RP17 PRELIMINARY; PRT; 322 AA.  
 ID Q9RP17; PRELIMINARY; PRT; 322 AA.  
 AC Q9RP17; PRELIMINARY; PRT; 322 AA.  
 DT 01-MAY-2000 (TREMBLrel. 13; Created)  
 DT 01-MAY-2001 (TREMBLrel. 16; Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22; Last annotation update)  
 DE HYCD.  
 GN HYCD.  
 OS Desulfobacterium dehalogenans.  
 CC Bacteria; Firmicutes; Clostridia; Clostridiales; Peptococcaceae.  
 OC Desulfobacterium.  
 RN [1] - TAXID=36554;  
 RP SEQUENCE OF 1-99 FROM N.A.  
 RX MEDLINE=20026799; PubMed=10559152;  
 RA Smidt H., Song D., van der Oost J., de Vos W.M.;  
 RT "Random transposition by Tn916 in *Desulfobacterium dehalogenans* allows for isolation and characterization of halorespiration-deficient mutants.";  
 RT J. Bacteriol. 181:6882-6888 (1999).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 CC -; SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.  
 DR EMBL; AF157639; AAF13042.2;  
 DR InterPro; IPR01694; RepB\_NADH\_dh1.  
 DR Pfam; PF00146; NADHdh\_1.  
 KW NAD; Oxidoreductase; Transmembrane.  
 SQ SEQUENCE 322 AA; 34620 MW; 91CAF4BAC3F96AB CRC64;  
 Query Match 2.6%; Score 8; DB 2; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DR 254 AVAILITL 261  
 Db 308 AVAILITL 315

RESULT 21  
 Q9C7E9 PRELIMINARY; PRT; 336 AA.  
 ID Q9C7E9; PRELIMINARY; PRT; 336 AA.  
 AC 09C7E9;  
 DR DT 01-JUN-2001 (TREMBLrel. 17; Created)  
 DR DT 01-JUN-2001 (TREMBLrel. 17; Last sequence update)  
 DR DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)

DE RING zinc finger protein, putative.  
 GN P13K9\_14.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 RN NCBI\_TaxID=3702;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 MEDLINE=21016719; PubMed=11130712;  
 RX Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,  
 RA White O., Alonso J., Altaji H., Araujo R., Bowman C.L., Brooks S.Y.,  
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,  
 RA Dunn P., Etxu P., Feldblyum T.V., Fong B., Fujii C.Y.,  
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.P., Hughes B., Huijar L.,  
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
 RA Kim C.J., Koo H.L., Kremenetskaya I., Kurtz D.B., Kwan A., Lam B.,  
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
 RA Lin X., Liu S.X., Liu Z.A., Luos J.S., Maiti R., Marziali A.,  
 RA Miltzschner J., Miranda M., Nguyen M., Nierman W.K., Osborne B.I.,  
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
 RA Sun H., Tallon L.J., Tambang G., Toriumi M.J., Town C.D.,  
 RA Utterback T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,  
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,  
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
 thaliana."  
 RL Nature 408:816-820(2000).  
 CC !- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL; AC089471; A0G51486\_1; -.  
 DR InterPro; IPR001841; Znf\_RING.  
 PFam; PF00097; zf-C2HC4\_1.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS50085; ZP RING\_2\_1.  
 DR Glycopro; Glycoprotein; Transmembrane.  
 SQ 336 AA; 37711 MW; 1218C9624BE2FB4B CRC64;  
 RESULT 22  
 Q9MXL5 PRELIMINARY; PRT; 338 AA.  
 ID Q9MXL5 PRELIMINARY; PRT; 338 AA.  
 AC 09MXL5;  
 DR 01-OCT-2000 (TREMBLrel. 15, Created)  
 DR 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DR 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE MHC class I antigen (Fragment).  
 GN PATR-C.  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelostomi;  
 OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.  
 NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 MEDLINE=20322475; PubMed=10866106;  
 RA de Groot N.G., Oting N., Arguello R., Watkins D.I., Doxiadis G.G.M.,  
 RA Madrigal J.A., Bontrop R.E.;  
 RT "Major histocompatibility complex class I diversity in a West African  
 chimpanzee population: implications for HIV research."  
 RL Immunogenetics 51:398-409(2000).  
 CC !- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE  
 CC IMMUNE SYSTEM (BY SIMILARITY).  
 CC !- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

CC MICROGLOBULIN (BY SIMILARITY).  
 DR EMBL; AF165373; AAP72772.1; -.  
 DR HSSP; P30685; 1A9E.  
 DR InterPro; IPR007110; Ig-like.  
 DR IPR003597; Ig\_L1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR001039; Ig\_C1.  
 DR Pfam; PF00047; Ig\_C1.  
 DR Pfam; PF00047; Ig\_C1.  
 DR PROSITE; PS50835; Ig\_LIKE; 1.  
 DR Glycopro; Glycoprotein; Transmembrane.  
 FT NON\_TER 1  
 SQ 348 AA; 38753 MW; 260F31IEBCDBFF620F CRC64;  
 RESULT 23  
 Q9MWAT9 PRELIMINARY; PRT; 348 AA.  
 ID Q9MWAT9 PRELIMINARY; PRT; 348 AA.  
 AC Q9MWAT9;  
 DR Q9MWAT9;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE MHC class I heavy chain antigen (Fragment).  
 DR GOGO-C.  
 GN OS Gorilla gorilla (gorilla).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelostomi;  
 OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Gorilla.  
 NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=21142798; PubMed=11207289;  
 RX PRT; 348 AA.  
 RA Urwater J.A., Hickman H., Dzuris J.L., Prilliman K., Allen T.M.,  
 RA Schwartz K.J., Lorentzen D., Shuflebotham C., Collins E.J.,  
 RA Neffler D.L., Raphael B., Hildebrand W., Sette A., Watkins D.I.;  
 RT "Gorillas with Spondyloarthropathies Express an MHC Class I Molecule  
 with Arginine at P2."  
 RT J. Immunol. 166:3334-3344 (2001).  
 RL CC IMMUNE SYSTEM (BY SIMILARITY).  
 CC !- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE  
 CC IMMUNE SYSTEM (BY SIMILARITY).  
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN (BY SIMILARITY).  
 DR EMBL; AF157411; AAP80354.1; -.  
 DR HSSP; P03989; 1HSA.  
 DR InterPro; IPR007110; Ig\_C1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR PROSITE; PS50835; Ig\_LIKE; 1.  
 DR Pfam; PF00047; Ig\_C1.  
 DR Pfam; PF00129; Ig\_C1.  
 DR PROSITE; PRO16388; WHCLASSI.  
 DR PRODom; PD00050; Ig\_C1.  
 DR SMART; SM00407; Ig\_C1.  
 DR PROSITE; PS50835; Ig\_LIKE; 1.  
 DR Glycopro; Glycoprotein; Transmembrane.  
 FT NON\_TER 1  
 SQ 348 AA; 38753 MW; 260F31IEBCDBFF620F CRC64;  
 RESULT 24  
 Q9MXL5 PRELIMINARY; PRT; 348 AA.  
 ID Q9MXL5 PRELIMINARY; PRT; 348 AA.  
 AC 09MXL5;  
 DR 01-OCT-2000 (TREMBLrel. 15, Created)  
 DR 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DR 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE MHC class I antigen (Fragment).  
 GN PATR-C.  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelostomi;  
 OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.  
 NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 MEDLINE=20322475; PubMed=10866106;  
 RA de Groot N.G., Oting N., Arguello R., Watkins D.I., Doxiadis G.G.M.,  
 RA Madrigal J.A., Bontrop R.E.;  
 RT "Major histocompatibility complex class I diversity in a West African  
 chimpanzee population: implications for HIV research."  
 RL Immunogenetics 51:398-409(2000).  
 CC !- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE  
 CC IMMUNE SYSTEM (BY SIMILARITY).  
 CC !- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

Qy	249 VLVVLAVL 256	DR	InterPro; IPR007110; Ig-like.
Db	307 VLVVLAVL 314	DR	InterPro; IPR003597; Ig_C1.
RESULT 24		DR	InterPro; IPR003006; Ig_MHC.
Q9PR46	PRELIMINARY;	PRT;	348 AA.
AC	Q9PR46	AC	InterPro; IPR001039; MHC_I.
DT	01-OCT-2000 (TRMBLrel. 15, Created)	DR	Pfam; PF00047; Ig; 1.
DT	01-OCT-2000 (TRMBLrel. 15, Last sequence update)	DR	Pfam; PF00129; MHC_I; 1.
DT	01-MAR-2003 (TRMBLrel. 23, Last annotation update)	DR	PRINTS; PR01638; MHCCLASSI.
DB	Type I restriction enzyme M protein (Fragment).	DR	ProdDom; PD000050; MHC_I; 1.
GN	HSDM-1, OR: UU098.	DR	SMART; SM00407; IgC1; 1.
OS	Ureaplasma parvum (Ureaplasma urealyticum biotype 1).	DR	PROSITE; PS50035; Ig_LIKE; 1.
OC	Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.	KW	Glycoprotein; MHC; Transmembrane.
OX	NCBI_TaxID:134821;	SEQUENCE	363 AA; 40262 MW; AA851E80336F24F8 CRC64;
RN	[1]	Query Match	2.6%; Score 8; DB 7; Length 363;
RP	SEQUENCE FROM N.A.	Best Local Similarity	100.0%; Pred. No. 17; Gaps 0;
RC	STRAIN:Servar 3;	Matches	8; Conservative 0; Mismatches 0; Indels 0;
RX	MEDLINE=20500219; PubMed=11049724;	Q9XR48	Query Match
RA	Glass J.I.; Lefkowitz E.J.; Glass J.S.; Heiner C.R.; Chen E.Y.,	ID	249 VLVVLAVL 256
RA	Caselli G.H.;	Q9XR48	PRELIMINARY;
RT	"The complete sequence of the mucosal pathogen Ureaplasma urealyticum.";	ID	VLVVLAVL 321
RL	Nature 407:757-762 (2000).	AC	PRT; 365 AA.
DR	EMBL: AE002110; AAF30504.1; -.	DT	01-NOV-1999 (TRMBLrel. 12, Created)
DR	InterPro; IPR004546; HsdM.	DT	01-NOV-1999 (TRMBLrel. 12, Last sequence update)
DR	InterPro; IPR003665; Methylase M.	DT	01-MAR-2003 (TRMBLrel. 23, Last annotation update)
DR	InterPro; IPR002296; N12N6_mTFrase.	DE	MHC class I antigen (Fragment).
DR	InterPro; IPR003356; N6_DNA_Mtase.	GN	POPC.
DR	InterPro; IPR002052; N6_Mtase.	OS	Pongo pygmaeus (Orangutan).
DR	InterPro; IPR000051; SAW_bind.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
DR	PF02506; Methylesterase; N6_Mtase; 1.	NCBI_TaxID=9600;	Mammalia; Bacteria; Primates; Catarrhini; Hominidae; Bongo.
DR	Pfam; PF02384; N6_Mtase; 1.	RN	SEQUENCE FROM N.A.
DR	PRINTS; PR00507; N12N6MTFrase.	RP	MEDLINE=9367395; PubMed=10436190;
DR	TIGRFAMs; TIGR00497; hsdM; 1.	RX	RA
DR	PROSITE; PS00092; N6_MTASE; 1.	RA	Adams E.J.; Thomson G.; Parham P.;
DR	Complete proteome.	RL	"Evidence for an HLA-C-like locus in the orangutan Pongo pygmaeus.";
RN	SEQUENCE 348 AA; 39547 MW; 8D776CB13681DB62 CRC64;	CC	CC
DR	Best Local Similarity 100.0%; Pred. No. 16;	CC	-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
Matches	8; Conservative 0; Mismatches 0; Indels 0;	CC	-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
KW	Score 8; DB 16; Length 348;	CC	MICROGLOBULIN) (BY SIMILARITY).
SEQUENCE	348 AA;	CC	EMBL: AF118897; AA028437.1; -.
Qy	123 RKEIDEIV 130	DR	HSSP; P30685; IgE.
Db	336 RKEIDEIV 343	DR	InterPro; IPR007110; Ig-like.
RESULT 25		DR	InterPro; IPR003597; Ig_C1.
Q9SHC2	PRELIMINARY;	DR	SMART; SM00407; IgC1; 1.
AC	Q9SHC2;	DR	PROSITE; PS50035; Ig_LIKE; 1.
DT	01-DEC-2001 (TRMBLrel. 19, Created)	DR	Glycoprotein; Transmembrane.
DT	01-DEC-2001 (TRMBLrel. 19, Last sequence update)	FT	NON_TER 1 1
DB	Major histocompatibility complex, class I, C.	SEQUENCE	365 AA; 40722 MW; 4C9BB3A18BB66F0B CRC64;
OS	Homo sapiens (Human).	Query Match	2.6%; Score 8; DB 7; Length 365;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	Best Local Similarity	100.0%; Pred. No. 17; Gaps 0;
OC	Mammalia; Bacteria; Primates; Catarrhini; Hominidae; Homo.	Matches	8; Conservative 0; Mismatches 0; Indels 0;
OX	NCBI_TaxID:9606;	RN	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.	RC	SEQUENCE FROM N.A. and Retinal pigment epithelium;
RA	Strainsberg R.;	RA	Submitted (MAY-2001) to the EMBL/GenBank/DDJB databases.
RL		CC	-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC		CC	IMMUNE SYSTEM (BY SIMILARITY).
CC		CC	-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC		CC	MICROGLOBULIN) (BY SIMILARITY).
EMBL; BC007814; AAH07814.1; -.	RESULTS	27	Q9XR48

ID	Q9XRX7	PRELIMINARY;	PRT;	365 AA.	DR	InterPro; IPR007110; Ig-like.
AC	Q9XRX7				DR	InterPro; IPR003597; Ig_C1.
DT	01-NOV-1999	(TRMBLref. 12, Last sequence update)			DR	InterPro; IPR003006; Ig_MHC.
DT	01-NOV-1999	(TRMBLref. 12, Last sequence update)			DR	InterPro; IPR001039; MHC_I.
DT	01-MAR-2003	(TRMBLref. 23, Last annotation update)			DR	InterPro; IPR00047; Ig_1.
DB	MHC class I antigen (Fragment).				DR	Pfam; PF00129; MHC_I; 1.
GN	POPY C.				DR	PRINTS; PRO1638; MHCCLASSI.
OS	Pongo pygmaeus (Orangutan).				DR	ProDom; PD000050; MHC_I; 1.
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.				DR	SMART; SM00407; IgC1; 1.
NCBI_TaxID	9600;				DR	PROSITE; PS50035; Ig_LIKE; 1.
RN	[1]				KW	Glycoprotein; Transmembrane.
RP	SEQUENCE FROM N.A.				FT	NON_TER 1
RX	MEDLINE=93167395; PubMed=10436180;				SEQUENCE	365 AA; 40813 MW; 51247CE97E8866E5 CRC64;
RA	Adams B.J.; Thomson G.; Parham P.;				Query Match	2.6%; Score 8; DB 7; Length 365;
RT	"Evidence for an HLA-C-like locus in the orangutan Pongo pygmaeus."				Best Local Similarity	100.0%; Pred. No. 17;
RL	Immunogenetics 49:865-871(1999).				Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
CC	-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).				Qy	249 VLVVLAVL 256
CC	-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).				Db	316 VLVVLAVL 323
CC	EMBL; AF118898; AD28438.1; -.					
DR	HSSP; P30685; 1A9E.					
DR	InterPro; IPR007110; Ig-like.					
DR	InterPro; IPR003597; Ig_C1.					
DR	InterPro; IPR003106; Ig_MHC.					
DR	InterPro; IPR001039; MHC_I.					
DR	Pfam; PF00047; Ig_1.					
DR	PRINTS; PRO1638; MHC_I; 1.					
DR	ProDom; PD000050; MHC_I; 1.					
DR	SMART; SM00407; IgC1; 1.					
DR	PROSITE; PS50035; Ig_LIKE; 1.					
DR	PROSITE; PS000230; Ig_MHC; 1.					
DR	Glycoprotein; Transmembrane.					
FT	NON_TER 1					
SEQUENCE	365 AA; 40613 MW; D3C078CFB226EB1D CRC64;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=9809975; PubMed=9433339;					
RA	Cooper S.L.; Adams B.J.; Wells R.S.; Walker C.M.; Parham P.;					
RA	RT "A major histocompatibility complex class I allele shared by two species of chimpanzee."					
RL	ProDom; PD000710; IgE.					
GN	PATR-C*0901.					
OS	Pan troglodytes (Chimpanzee), and Pan paniscus (Pygmy chimpanzee) (Bonobo).					
OS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.					
NCBI_TaxID	9598; 9597;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=9809975; PubMed=9433339;					
RA	Cooper S.L.; Adams B.J.; Wells R.S.; Walker C.M.; Parham P.;					
RA	RT "A major histocompatibility complex class I allele shared by two species of chimpanzee."					
RL	ProDom; PD000710; IgE.					
GN	PATR-C*0901.					
OS	ImmunoGenetics 47:212-217(1998).					
CC	-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).					
CC	-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).					
CC	EMBL; AJ001976; CA005124.1; -.					
DR	EMBL; AJ001973; CA005123.1; -.					
DR	EMBL; AJ001973; CA005122.1; -.					
DR	EMBL; AJ001974; CA005122.1; -.					
DR	HSSP; P30685; IgE.					
DR	InterPro; IPR007110; Ig_LIKE.					
DR	InterPro; IPR003597; Ig_C1.					
DR	InterPro; IPR003006; Ig_MHC.					
DR	SMART; SM00407; IgC1; 1.					
DR	PROSITE; PS50035; Ig_LIKE; 1.					
DR	Glycoprotein; Transmembrane.					
FT	NON_TER 1					
SEQUENCE	366 AA; 40965 MW; 422959BD8CC9C01 CRC64;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	Adams E.J.; Cooper S.; Thomson G.; Parham P.;					
RT	"Common Chimpanzees have Greater Diversity than Humans at Two of the Three Highly Polymorphic MHC Class I Genes."					
RT	Immunogenetics 51:410-424(2000).					
CC	-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).					
CC	-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).					
DR	EMBL; AF119672; AAF7694.1; -.					
DR	HSSP; P30685; 1A9E.					

RESULT 30	Q8MMH0	PRELIMINARY;	PRT;	366 AA.	CC EMBL; AJ010749; CAA09341.1; -.
ID Q8MMH0;	DR HSSP; P30460; IAGD.	DR InterPro; IPR007110; Ig-like.	DR		DR HSSP; P30460; IAGD.
AC 08MMH0;	DR InterPro; IPR003597; Ig_C1.	DR InterPro; IPR003006; Ig_MHC.	DR		DR InterPro; IPR003597; Ig_C1.
DT 01-OCT-2002 (TREMBLrel. 22, Created)	DR InterPro; IPR001039; MHC_I.	DR InterPro; IPR001039; MHC_I.	DR		DR InterPro; IPR001039; MHC_I.
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	DR Pfam; PF00047; Ig_1.	DR Pfam; PF00129; MHC_I.	DR		DR Pfam; PF00129; MHC_I.
DB MHC Class I antigen.	DR PRINTS; PRO1638; MHCCLASSI.	DR PRINTS; PRO1638; MHCCLASSI.	DR		DR PRINTS; PRO1638; MHCCLASSI.
GN P0P-C.	DR ProDom; PD000050; MHC_I.	DR SMART; SM00407; IgCl_1.	DR		DR ProDom; PD000050; MHC_I.
OS Pongo pygmaeus (Orangutan).	DR PROSITE; PS50835; Ig_LIKE; 1.	DR PROSITE; PS50835; Ig_LIKE; 1.	DR		DR PROSITE; PS50835; Ig_LIKE; 1.
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DR Glycoprotein; Signal; Transmembrane.	DR Glycoprotein; Signal; Transmembrane.	DR		DR Glycoprotein; Signal; Transmembrane.
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.	FT SIGNAL; 1 24 POTENTIAL.	FT SIGNAL; 1 24 POTENTIAL.	FT		FT SIGNAL; 1 24 POTENTIAL.
OX NCBI_TaxID:9600;	FT CHAIN 25 366 HLA CLASS I ANTIGEN.	FT CHAIN 25 366 HLA CLASS I ANTIGEN.	FT		FT CHAIN 25 366 HLA CLASS I ANTIGEN.
RN [1] SEQUENCE FROM N.A.	SQ SEQUENCE = 40789 MW; 4073C3A023E55DOC CRC64;	SQ SEQUENCE = 40789 MW; 4073C3A023E55DOC CRC64;	SQ		SQ SEQUENCE = 40789 MW; 4073C3A023E55DOC CRC64;
RX MEDLINE=22072192; PubMed=12077248;	CC FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).	CC FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).	CC		CC FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).
RA Guethlein L.A.; Plodin L.R.; Adams E.J.; Parham P.; RT Species for Tracking the Evolution of Killer Cell Ig-Like Receptors with MHC-C.";	RT Species for Tracking the Evolution of Killer Cell Ig-Like Receptors with MHC-C.";	RT Species for Tracking the Evolution of Killer Cell Ig-Like Receptors with MHC-C.";	RT		RT Species for Tracking the Evolution of Killer Cell Ig-Like Receptors with MHC-C.";
RL J. Immunol. 169:220-229 (2002).	RL J. Immunol. 169:220-229 (2002).	RL J. Immunol. 169:220-229 (2002).	RL		RL J. Immunol. 169:220-229 (2002).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).	CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).	CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).	CC		CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).	DR EMBL; AF403777; AMAP8477.1; -.	DR EMBL; AF403777; AMAP8477.1; -.	DR		DR EMBL; AF403777; AMAP8477.1; -.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).	DR InterPro; IPR007110; Ig-like.	DR InterPro; IPR007110; Ig-like.	DR		DR InterPro; IPR007110; Ig-like.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).	DR InterPro; IPR003597; Ig_C1.	DR InterPro; IPR003597; Ig_C1.	DR		DR InterPro; IPR003597; Ig_C1.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).	DR InterPro; IPR003006; Ig_MHC.	DR InterPro; IPR003006; Ig_MHC.	DR		DR InterPro; IPR003006; Ig_MHC.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).	DR Pfam; PF00047; Ig_1.	DR Pfam; PF00129; MHC_I; 1.	DR		DR Pfam; PF00129; MHC_I; 1.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).	DR PRINTS; PRO1638; MHCCLASSI.	DR PRINTS; PRO1638; MHCCLASSI.	DR		DR PRINTS; PRO1638; MHCCLASSI.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).	DR ProDom; PD000050; MHC_I.	DR ProDom; PD000050; MHC_I.	DR		DR ProDom; PD000050; MHC_I.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).	DR SMART; SM00407; IgCl_1.	DR SMART; SM00407; IgCl_1.	DR		DR SMART; SM00407; IgCl_1.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).	DR PROSITE; PS50835; Ig_LIKE; 1.	DR PROSITE; PS50835; Ig_LIKE; 1.	DR		DR PROSITE; PS50835; Ig_LIKE; 1.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).	DR Glycoprotein; Transmembrane.	DR Glycoprotein; Transmembrane.	DR		DR Glycoprotein; Transmembrane.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).	SQ SEQUENCE . 366 AA; 40672 MW; 05DC89FAD0DB831A CRC64;	SQ SEQUENCE . 366 AA; 40672 MW; 05DC89FAD0DB831A CRC64;	SQ		SQ SEQUENCE . 366 AA; 40672 MW; 05DC89FAD0DB831A CRC64;
RESULT 31	Q9TQP9	PRELIMINARY;	PRT;	366 AA.	CC TISSUE=Melanoma;
ID Q9TQP9;	CC Coulie P.G.;	CC "Identification of a new HLA-Cw7 allele.";	RN [1] SEQUENCE FROM N.A.		CC Coulie P.G.;
AC Q9TQP9;	CC RLSubmitted (MAY-1994) to the EMBL/GenBank/DBJ databases.	CC "Identification of a new HLA-Cw7 allele.";	RN [1] SEQUENCE FROM N.A.		CC RLSubmitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
DT 01-MAY-2000 (TREMBLrel. 13, Created)	CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).	CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).	RN [1] SEQUENCE FROM N.A.		CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).	CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).	RN [1] SEQUENCE FROM N.A.		CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	DR Pfam; PF00047; Ig_1.	DR Pfam; PF00129; MHC_I; 1.	DR		DR Pfam; PF00047; Ig_1.
DB HLA-Cw*070X.	DR PRINTS; PRO1638; MHCCLASSI.	DR PRINTS; PRO1638; MHCCLASSI.	DR		DR PRINTS; PRO1638; MHCCLASSI.
GN HLA-Cw*070X.	DR ProDom; PD000050; MHC_I.	DR ProDom; PD000050; MHC_I.	DR		DR ProDom; PD000050; MHC_I.
OS Homo sapiens (Human).	DR SMART; SM00407; IgCl_1.	DR SMART; SM00407; IgCl_1.	DR		DR SMART; SM00407; IgCl_1.
CC Homo sapiens (Human).	DR PROSITE; PS50835; Ig_LIKE; 1.	DR PROSITE; PS50835; Ig_LIKE; 1.	DR		DR PROSITE; PS50835; Ig_LIKE; 1.
CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	DR Glycoprotein; Transmembrane.	DR Glycoprotein; Transmembrane.	DR		DR Glycoprotein; Transmembrane.
OX NCBI_TaxID:9606;	DR HSSP; P30460; IAGD.	DR HSSP; P30460; IAGD.	DR		DR HSSP; P30460; IAGD.
RN [1] SEQUENCE FROM N.A.	CC TISSUE=Melanoma;	CC TISSUE=Melanoma;	RN [1] SEQUENCE FROM N.A.		CC TISSUE=Melanoma;
RX MEDLINE=99299762; PubMed=10372547;	CC Coulie P.G./	CC "Correction of HLA-Cw*0501 and identification of HLA-Cw*0711.";	RN [1] SEQUENCE FROM N.A.		CC Coulie P.G./
RA Baurain J.P., Coulie P.G./	CC Tissue Antigens 53:510-512 (1999).	CC Tissue Antigens 53:510-512 (1999).	RN [1] SEQUENCE FROM N.A.		CC Tissue Antigens 53:510-512 (1999).
RT "Correction of HLA-Cw*0501 and identification of HLA-Cw*0711.";	CC IMMUNE SYSTEM (BY SIMILARITY).	CC IMMUNE SYSTEM (BY SIMILARITY).	RN [1] SEQUENCE FROM N.A.		CC IMMUNE SYSTEM (BY SIMILARITY).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).	CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).	CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).	RN [1] SEQUENCE FROM N.A.		CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).	DR SEQUENCE = 40847 MW; 63321EC0158049B6 CRC64;	DR SEQUENCE = 40847 MW; 63321EC0158049B6 CRC64;	SQ		DR SEQUENCE = 40847 MW; 63321EC0158049B6 CRC64;
RESULT 32	Q29652	PRELIMINARY;	PRT;	366 AA.	CC TISSUE=Melanoma;
ID Q29652;	CC RLSubmitted (MAY-1994) to the EMBL/GenBank/DBJ databases.	CC "Identification of a new HLA-Cw7 allele.";	RN [1] SEQUENCE FROM N.A.		CC RLSubmitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
AC Q29652;	CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).	CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).	RN [1] SEQUENCE FROM N.A.		CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).
DT 01-NOV-1996 (TREMBLrel. 01, Created)	DR HLA-Cw7.	DR HLA-Cw7.	DR		DR HLA-Cw7.
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)	DR Pfam; PF00047; Ig_1.	DR Pfam; PF00129; MHC_I; 1.	DR		DR Pfam; PF00047; Ig_1.
DR SMART; SM00407; IgCl_1.	DR PRINTS; PRO1638; MHCCLASSI.	DR PRINTS; PRO1638; MHCCLASSI.	DR		DR PRINTS; PRO1638; MHCCLASSI.
DR PROSITE; PS50835; Ig_LIKE; 1.	DR ProDom; PD000050; MHC_I.	DR ProDom; PD000050; MHC_I.	DR		DR ProDom; PD000050; MHC_I.
DR Glycoprotein; Transmembrane.	DR SMART; SM00407; IgCl_1.	DR SMART; SM00407; IgCl_1.	DR		DR SMART; SM00407; IgCl_1.
DR HSSP; P30460; IAGD.	DR Glycoprotein; Transmembrane.	DR Glycoprotein; Transmembrane.	DR		DR Glycoprotein; Transmembrane.
RN [1] SEQUENCE FROM N.A.	CC TISSUE=Melanoma;	CC TISSUE=Melanoma;	RN [1] SEQUENCE FROM N.A.		CC TISSUE=Melanoma;
RX MEDLINE=99299762; PubMed=10372547;	CC Coulie P.G./	CC "Correction of HLA-Cw*0501 and identification of HLA-Cw*0711.";	RN [1] SEQUENCE FROM N.A.		CC Coulie P.G./
RA Baurain J.P., Coulie P.G./	CC Tissue Antigens 53:510-512 (1999).	CC Tissue Antigens 53:510-512 (1999).	RN [1] SEQUENCE FROM N.A.		CC Tissue Antigens 53:510-512 (1999).
RT "Correction of HLA-Cw*0501 and identification of HLA-Cw*0711.";	CC IMMUNE SYSTEM (BY SIMILARITY).	CC IMMUNE SYSTEM (BY SIMILARITY).	RN [1] SEQUENCE FROM N.A.		CC IMMUNE SYSTEM (BY SIMILARITY).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).	CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).	CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).	RN [1] SEQUENCE FROM N.A.		CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).	DR SEQUENCE = 40847 MW; 63321EC0158049B6 CRC64;	DR SEQUENCE = 40847 MW; 63321EC0158049B6 CRC64;	SQ		DR SEQUENCE = 40847 MW; 63321EC0158049B6 CRC64;
RESULT 33	Q9TQP9	PRELIMINARY;	PRT;	366 AA.	CC TISSUE=Melanoma;
ID Q9TQP9;	CC Coulie P.G.;	CC "Identification of a new HLA-Cw7 allele.";	RN [1] SEQUENCE FROM N.A.		CC Coulie P.G.;
AC Q9TQP9;	CC RLSubmitted (MAY-1994) to the EMBL/GenBank/DBJ databases.	CC "Identification of a new HLA-Cw7 allele.";	RN [1] SEQUENCE FROM N.A.		CC RLSubmitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
DT 01-MAY-2000 (TREMBLrel. 13, Created)	DR Pfam; PF00047; Ig_1.	DR Pfam; PF00129; MHC_I; 1.	DR		DR Pfam; PF00047; Ig_1.
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	DR PRINTS; PRO1638; MHCCLASSI.	DR PRINTS; PRO1638; MHCCLASSI.	DR		DR PRINTS; PRO1638; MHCCLASSI.
DB HLA-Cw*070X.	DR ProDom; PD000050; MHC_I.	DR ProDom; PD000050; MHC_I.	DR		DR ProDom; PD000050; MHC_I.
GN HLA-Cw*070X.	DR SMART; SM00407; IgCl_1.	DR SMART; SM00407; IgCl_1.	DR		DR SMART; SM00407; IgCl_1.
OS Homo sapiens (Human).	DR PROSITE; PS50835; Ig_LIKE; 1.	DR PROSITE; PS50835; Ig_LIKE; 1.	DR		DR PROSITE; PS50835; Ig_LIKE; 1.
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	DR Glycoprotein; Transmembrane.	DR Glycoprotein; Transmembrane.	DR		DR Glycoprotein; Transmembrane.
OX NCBI_TaxID:9606;	DR HSSP; P30460; IAGD.	DR HSSP; P30460; IAGD.	DR		DR HSSP; P30460; IAGD.
RN [1] SEQUENCE FROM N.A.	CC TISSUE=Melanoma;	CC TISSUE=Melanoma;	RN [1] SEQUENCE FROM N.A.		CC TISSUE=Melanoma;
RX MEDLINE=99299762; PubMed=10372547;	CC Coulie P.G./	CC "Correction of HLA-Cw*0501 and identification of HLA-Cw*0711.";	RN [1] SEQUENCE FROM N.A.		CC Coulie P.G./
RA Baurain J.P., Coulie P.G./	CC Tissue Antigens 53:510-512 (1999).	CC Tissue Antigens 53:510-512 (1999).	RN [1] SEQUENCE FROM N.A.		CC Tissue Antigens 53:510-512 (1999).
RT "Correction of HLA-Cw*0501 and identification of HLA-Cw*0711.";	CC IMMUNE SYSTEM (BY SIMILARITY).	CC IMMUNE SYSTEM (BY SIMILARITY).	RN [1] SEQUENCE FROM N.A.		CC IMMUNE SYSTEM (BY SIMILARITY).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).	CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).	CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).	RN [1] SEQUENCE FROM N.A.		CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).	DR SEQUENCE = 40847 MW; 63321EC0158049B6 CRC64;	DR SEQUENCE = 40847 MW; 63321EC0158049B6 CRC64;	SQ		DR SEQUENCE = 40847 MW; 63321EC0158049B6 CRC64;

RESULT 33	Q95463	PRELIMINARY;	PRT;	366 AA.	CC	MICROGLOBULIN (BY SIMILARITY).
ID	Q95463				DR	EMBL; AF470376; AAC78476.1; -.
AC	Q95463;				DR	InterPro; IPR007110; Ig-like.
DT	01-FEB-1997	(TREMBLrel. 02, Created)			DR	InterPro; IPR03597; Ig_C1.
DT	01-FEB-1997	(TREMBLrel. 02, Last sequence update)			DR	InterPro; IPR003006; Ig_MHC.
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)			DR	InterPro; IPR001039; MHC_I.
DB	HLA-C Protein precursor.				PFam;	PF00047; Ig; 1.
GN	HLA-C				DR	PFam; PF00119; MHC_I; 1.
GN	HLA-CW*07GB.				DR	PRINTS; PR01638; MHCCLASSI.
OS	Homo sapiens (Human)				DR	ProDom; PD000050; MHC_I; 1.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				DR	SMART; SM00407; IgC1; 1.
OC	Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.				DR	PROSITE; PS50335; Ig_LIKE; 1.
OX	NCBI_TaxID=9606;				DR	PROSITE; PS00390; Ig_MHC; 1.
RN	[1]				KW	Glycoprotein; Transmembrane.
RP	SEQUENCE FROM N.A.				SEQUENCE	366 AA; 40853 MW; 3112BC758471B1EC CRC64;
RX	Medline=97161041; PubMed=2008313;				Query Match	2.6%; Score 8; DB 7; Length 366;
RA	Vilches C., Bunce M., Sanz L., de Pablo R., Puente S., Kreisler M.;				Best Local Similarity	100.0%; Pred. No. 17;
RT	"Molecular cloning of two new HLA-C alleles: Cw*1501 and Cw*0706.";				Matches	0; Mismatches 0; Indels 0; Gaps 0;
RL	Tissue Antigens 48:698-702(1996).					
CC	-!- FUNCTION INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).					
CC	-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-CC MICROGLOBULIN) (BY SIMILARITY).					
DR	EMBL; X97321; CAA65986.1; -.					
DR	HSSP; P30605; 1A9E.					
DR	InterPro; IPR007110; Ig-like.					
DR	InterPro; IPR003597; Ig_C1.					
DR	InterPro; IPR003006; Ig_MHC.					
DR	InterPro; IPR001039; MHC_I.					
DR	PFam; PF00047; Ig; 1.					
DR	PFam; PF00129; MHC_I; 1.					
DR	PRINTS; PR01638; MHCCLASSI.					
DR	ProDom; PD000050; MHC_I; 1.					
DR	SMART; SM00407; IgC1; 1.					
DR	PROSITE; PS50335; Ig_LIKE; 1.					
KW	Glycoprotein; Signal; Transmembrane.					
FT	SIGNAL 1 24 POTENTIAL.					
FT	CHAIN 25 366 POTENTIAL.					
SQ	SEQUENCE 366 AA; 40735 MW; 0B95050400280609 CRC64;					
RP	SEQUENCE FROM N.A.				RP	SEQUENCE FROM N.A.
RX	Medline=22072192; PubMed=1207248;				RX	Medline=22072192; PubMed=1207248;
RA	Guehlein L.A., Flodin L.R., Adams E.J., Parham P.;				RA	Guehlein L.A., Flodin L.R., Adams E.J., Parham P.;
RT	"NK Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors with MHC-C."				RT	"NK Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors with MHC-C."
RT	-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).				RT	-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).
CC	-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-CC MICROGLOBULIN) (BY SIMILARITY).				CC	-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-CC MICROGLOBULIN) (BY SIMILARITY).
CC	-!- DR EMBL; AF470379; AAC78479.1; -.				CC	-!- DR EMBL; AF470379; AAC78479.1; -.
DR	InterPro; IPR007110; Ig-like.				DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig_C1.				DR	InterPro; IPR003597; Ig_C1.
DR	InterPro; IPR003006; Ig_MHC.				DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR001039; MHC_I.				DR	InterPro; IPR001039; MHC_I.
DR	PFam; PF00047; Ig; 1.				DR	PFam; PF00047; Ig; 1.
DR	PFam; PF00129; MHC_I; 1.				DR	PFam; PF00129; MHC_I; 1.
DR	PRINTS; PR01638; MHCCLASSI.				DR	PRINTS; PR01638; MHCCLASSI.
DR	ProDom; PD000050; MHC_I.				DR	ProDom; PD000050; MHC_I.
DR	SMART; SM00407; IgC1; 1.				DR	SMART; SM00407; IgC1; 1.
DR	PROSITE; PS50335; Ig_LIKE; 1.				DR	PROSITE; PS50335; Ig_LIKE; 1.
KW	Glycoprotein; Transmembrane.				DR	PROSITE; PS00290; Ig_MHC; 1.
SEQUENCE	366 AA; 40890 MW; 743AEFB8A8624922D CRC64;				DR	SEQUENCE 366 AA; 40890 MW; 743AEFB8A8624922D CRC64;
RP	SEQUENCE FROM N.A.				Query Match	2.6%; Score 8; DB 7; Length 366;
RX	Medline=22072192; PubMed=1207248;				Best Local Similarity	100.0%; Pred. No. 17;
RA	Guehlein L.A., Flodin L.R., Adams E.J., Parham P.;				Matches	0; Mismatches 0; Indels 0; Gaps 0;
RT	"NK Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors with MHC-C."					
RT	-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).					
CC	-!- DR EMBL; AF470379; AAC78479.1; -.					
CC	-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-CC MICROGLOBULIN) (BY SIMILARITY).					
CC	-!- DR EMBL; AF470379; AAC78479.1; -.					
DR	InterPro; IPR007110; Ig-like.				Query Match	2.6%; Score 8; DB 7; Length 366;
DR	InterPro; IPR003597; Ig_C1.				Best Local Similarity	100.0%; Pred. No. 17;
DR	InterPro; IPR003006; Ig_MHC.				Matches	0; Mismatches 0; Indels 0; Gaps 0;
DR	InterPro; IPR001039; MHC_I.					
DR	PFam; PF00047; Ig; 1.					
DR	PFam; PF00129; MHC_I; 1.					
DR	PRINTS; PR01638; MHCCLASSI.					
DR	ProDom; PD000050; MHC_I.					
DR	SMART; SM00407; IgC1; 1.					
DR	PROSITE; PS50335; Ig_LIKE; 1.					
KW	Glycoprotein; Transmembrane.					
SEQUENCE	366 AA; 40890 MW; 743AEFB8A8624922D CRC64;					
RP	SEQUENCE FROM N.A.					
RX	Medline=169-220-229 (2002).					
RA	J. Immunol. 169:220-229 (2002).					
RT	"Immuno. 169:220-229 (2002).					
RT	-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).					
CC	-!- DR EMBL; AF470379; AAC78479.1; -.					
CC	-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-CC MICROGLOBULIN) (BY SIMILARITY).					
CC	-!- DR EMBL; AF470379; AAC78479.1; -.					
DR	InterPro; IPR007110; Ig-like.					
DR	InterPro; IPR003597; Ig_C1.					
DR	InterPro; IPR003006; Ig_MHC.					
DR	InterPro; IPR001039; MHC_I.					
DR	PFam; PF00047; Ig; 1.					
DR	PFam; PF00129; MHC_I; 1.					
DR	PRINTS; PR01638; MHCCLASSI.					
DR	ProDom; PD000050; MHC_I.					
DR	SMART; SM00407; IgC1; 1.					
DR	PROSITE; PS50335; Ig_LIKE; 1.					
KW	Glycoprotein; Transmembrane.					
SEQUENCE	366 AA; 40890 MW; 743AEFB8A8624922D CRC64;					
RP	SEQUENCE FROM N.A.					
RX	Medline=22072192; PubMed=1207248;					
RA	Guehlein L.A., Flodin L.R., Adams E.J., Parham P.;					
RT	"NK Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors with MHC-C."					
RT	-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).					
CC	-!- DR EMBL; AF470379; AAC78479.1; -.					
CC	-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-CC MICROGLOBULIN) (BY SIMILARITY).					
CC	-!- DR EMBL; AF470379; AAC78479.1; -.					
DR	InterPro; IPR007110; Ig-like.				Query Match	2.6%; Score 8; DB 7; Length 366;
DR	InterPro; IPR003597; Ig_C1.				Best Local Similarity	100.0%; Pred. No. 17;
DR	InterPro; IPR003006; Ig_MHC.				Matches	0; Mismatches 0; Indels 0; Gaps 0;
DR	InterPro; IPR001039; MHC_I.					
DR	PFam; PF00047; Ig; 1.					
DR	PFam; PF00129; MHC_I; 1.					
DR	PRINTS; PR01638; MHCCLASSI.					
DR	ProDom; PD000050; MHC_I.					
DR	SMART; SM00407; IgC1; 1.					
DR	PROSITE; PS50335; Ig_LIKE; 1.					
KW	Glycoprotein; Transmembrane.					
SEQUENCE	366 AA; 40890 MW; 743AEFB8A8624922D CRC64;					
RP	SEQUENCE FROM N.A.					
RX	Medline=22072192; PubMed=1207248;					
RA	Guehlein L.A., Flodin L.R., Adams E.J., Parham P.;					
RT	"NK Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors with MHC-C."					
RT	-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).					
CC	-!- DR EMBL; AF470379; AAC78479.1; -.					
CC	-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-CC MICROGLOBULIN) (BY SIMILARITY).					
CC	-!- DR EMBL; AF470379; AAC78479.1; -.					
DR	InterPro; IPR007110; Ig-like.				Query Match	2.6%; Score 8; DB 7; Length 366;
DR	InterPro; IPR003597; Ig_C1.				Best Local Similarity	100.0%; Pred. No. 17;
DR	InterPro; IPR003006; Ig_MHC.				Matches	0; Mismatches 0; Indels 0; Gaps 0;
DR	InterPro; IPR001039; MHC_I.					
DR	PFam; PF00047; Ig; 1.					
DR	PFam; PF00129; MHC_I; 1.					
DR	PRINTS; PR01638; MHCCLASSI.					
DR	ProDom; PD000050; MHC_I.					
DR	SMART; SM00407; IgC1; 1.					
DR	PROSITE; PS50335; Ig_LIKE; 1.					
KW	Glycoprotein; Transmembrane.					
SEQUENCE	366 AA; 40890 MW; 743AEFB8A8624922D CRC64;					
RP	SEQUENCE FROM N.A.					
RX	Medline=169-220-229 (2002).					
RA	J. Immunol. 169:220-229 (2002).					
RT	"Immuno. 169:220-229 (2002).					
RT	-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).					
CC	-!- DR EMBL; AF470379; AAC78479.1; -.					
CC	-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-CC MICROGLOBULIN) (BY SIMILARITY).					
CC	-!- DR EMBL; AF470379; AAC78479.1; -.					
DR	InterPro; IPR007110; Ig-like.				Query Match	2.6%; Score 8; DB 7; Length 366;
DR	InterPro; IPR003597; Ig_C1.				Best Local Similarity	100.0%; Pred. No. 17;
DR	InterPro; IPR003006; Ig_MHC.				Matches	0; Mismatches 0; Indels 0; Gaps 0;
DR	InterPro; IPR001039; MHC_I.					
DR	PFam; PF00047; Ig; 1.					
DR	PFam; PF00129; MHC_I; 1.					
DR	PRINTS; PR01638; MHCCLASSI.					
DR	ProDom; PD000050; MHC_I.					
DR	SMART; SM00407; IgC1; 1.					
DR	PROSITE; PS50335; Ig_LIKE; 1.					
KW	Glycoprotein; Transmembrane.					
SEQUENCE	366 AA; 40890 MW; 743AEFB8A8624922D CRC64;					



DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Glycoprotein; Transmembrane;  
SEQUENCE 366 AA; 40665 MW; 00E0836EB2FEC4A2 CRC64;

Query Match 2.6%; Score 8; DB 7; Length 366;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 249 VLVVLAVL 256  
Db 317 VLVVLAVL 324

RESULT 39  
Q29865 PRELIMINARY; PRT; 366 AA.  
AC Q29865\_01; Created  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
OS Homo sapiens (Human)  
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.  
NCBI\_TaxID:9606;  
RN [1]  
RP SEQUENCE FROM N.A.

AC Q95603; 02; Created  
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
DT 01-FEB-1997 (TREMBLrel. 02, Last annotation update)  
DE HLA-CW\*0702 (Human Leucocyte Antigen C).  
GN HLA-CW\*0702.  
OS Homo sapiens (Human)  
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.  
NCBI\_TaxID:9606;  
RN [1]  
RP TISSUE=Blood;  
RX MEDLINE=96232973; PubMed=8655361;  
RA Wang H., Tokunaga K., Ishikawa Y., Asahina A., Kuwata S., Akaza T.,  
RA Tadokoro K., Shibata Y., Takiguchi M., Juji T.;  
RT "Identification and DNA typing of two Cw7 alleles (Cw\*0702 and  
Cw\*0704) in Japanese with the corrected sequence of Cw\*0702.";  
RT Cw\*0704  
RL Human. Immunol. 45:52-58(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Cox S.T., Mcwhinny A.J., Little A.M.;  
RT "New HLA sequences with intron 2 differences.";  
RL Submitted (AUG-2000) to the ENBL/GenBank/DBJ databases.  
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE  
CC IMMUNE SYSTEM (BY SIMILARITY)  
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
RN MICROGLOBULIN) (BY SIMILARITY).  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97161041; PubMed=9008313;  
RA Vilches C., Bunce M., Sanz L., de Pablo R., Puente S., Kreisler M.;  
OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.  
OX NCBI\_TaxID:9606;  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Cox S.T.;  
RT "Full genomic sequence alignments for HLA-B and -C.";  
RL Submitted (NOV-2001) to the ENBL/GenBank/DBJ databases.  
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE  
CC IMMUNE SYSTEM (BY SIMILARITY).  
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
RN MICROGLOBULIN) (BY SIMILARITY).  
CC -!- PROSITE: PS50835; IG\_LIKE; 1.  
DR EMBL; X96582; CRAE6401.1; -.  
DR HSSP; P3065; CAD12438.1; -.  
DR PFAM; PF00047; Ig; 1.  
DR PFAM; PF00129; Ig; 1.  
DR PFAM; PF00460; IgA2.  
DR PRINTS; PRO007110; Ig-1-like.  
DR InterPro; IPR003597; Ig-c1.  
DR InterPro; IPR003006; Ig-MHC.  
DR InterPro; IPR001039; MHC\_I.  
DR PFAM; PF00047; Ig; 1.  
DR PRODOM; PD000050; MHC\_I.  
DR SMART; SM00407; IgC1; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
DR PROSITE; PS00290; Ig\_MHC; 1.  
KW Glycoprotein; Signal; Transmembrane.  
FT SIGNAL 1 24 POTENTIAL.  
FT CHAIN 25 366 POTENTIAL.  
SQ SEQUENCE 366 AA; 40933 MW; 67C87E948E4327D8 CRC64;

Query Match 2.6%; Score 8; DB 7; Length 366;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 249 VLVVLAVL 256  
Db 317 VLVVLAVL 324

RESULT 41  
Q9TPL2 PRELIMINARY; PRT; 366 AA.  
ID Q9TPL2; PRELIMINARY; PRT;  
AC 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-0003 (TREMBLrel. 23, Last annotation update)  
DB MHC class I antigen (Lymphocyte antigen).  
GN HLA-C OR PATR-C OR PATR-C04;  
OS Pan troglodytes (Chimpanzee).  
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarhini; Hominidae; Pan.  
NCBI\_TaxID:9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=36C-1;  
RX MEDLINE=99335357; PubMed=10405321;  
RA Matsui M., Machida S., Feinstone S.M., Akatsuwa T.;

RESULT 40  
Q95603 PRELIMINARY; PRT; 366 AA.  
ID Q95603 PRELIMINARY; PRT; 366 AA.

"Molecular analyses of five new chimpanzee MHC class I alleles: implications for differences between evolutionary mechanisms of HLA-A, B, and -C loci." ; Biochem. Biophys. Res. Commun. 261:46-52 (1999). [2]

SEQUENCE FROM N.A.  
MEDLINE=20122476; PubMed=10866107;  
Adams E.J., Cooper S., Thomson G., Parham P.; "Common Chimpanzees have Greater Diversity than Humans at Two of the Three Highly Polymorphic MHC Class I Genes." ; Immunogenetics 51:410-424 (2000). [3]

SEQUENCE FROM N.A.  
TISSUE=Blood;  
MEDLINE=20122475; PubMed=10866106;  
de Groot N.G., Otting N., Arguello R., Watkins D.I., Doxiadis G.G.M., Madrigal J.A., Bontrop R.E.; "Major histocompatibility complex class I diversity in a West African chimpanzee population: implications for HIV research." ; Immunogenetics 51:398-409 (2000). [4]

[1] SEQUENCE FROM N.A.  
 RP RP  
 RX RX PubMed=10866107;  
 RA RA MEDLINE=20132476; PubMed=10866107;  
 Adams B.J., Cooper S., Thomson G., Parham P.;  
 RT "Common Chimpanzees have Greater Diversity than Humans at Two of the  
 Three Highly Polymorphic MHC Class I Genes.",  
 RT Immunogenetics 51:410-424 (2000).  
 RL RL  
 RN RN  
 SEQUENCE FROM N.A.  
 RP RP  
 RC RC TISSUE=Blood;  
 RX RX PubMed=10866106;  
 RA RA MEDLINE=20132475; PubMed=10866106;  
 de Groot N.G., Ontong N., Arguello R., Watkins D.I., Doxakis G.G.M.,  
 RA RA Madrigal J.A., Bontrop R.E.;  
 RT RT "Major histocompatibility complex class I diversity in a West African  
 chimpanzee population: implications for HIV research.",  
 RT RT Immunogenetics 51:398-409 (2000).  
 RL RL  
 CC CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE  
 CC CC IMMUNE SYSTEM (BY SIMILARITY).  
 CC CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC CC -1- MICROGLOBULIN) (BY SIMILARITY).

SEQUENCE FROM N.A.  
STRAIN-Chimpanzee 458;  
Walker H., Erickson A.L., Cooper S., Domena J., Parham P.,  
Walker C.M.;  
"patr-A and B, the orthologues of HLA-A and B, present Hepatitis C  
virus epitopes to CD8 cytotoxic T cells from two chronologically  
infected chimpanzees.";  
Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
-1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE  
IMMUNE SYSTEM (BY SIMILARITY)  
-1- SUBUNIT: DIMER: ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
MICROGLOBULIN) (BY SIMILARITY).

EMBL; AF165366; AAF72765.1; -.  
 HSSP; P3058; 1AE8.  
 InterPro; IPR007110; Ig-like.  
 InterPro; IPR003006; Ig MHC.  
 InterPro; IPR01039; MHC\_I.  
 Pfam; PF00047; iq; 1.  
 Pfam; PF00129; MHC\_I; 1.  
 PRINTS; PRO1638; MHCC1SSI.  
 ProDom; PD00050; MHC\_I; 1.  
 PROSITE; PS50835; IG\_EIGE; 1.  
 Glycoprotein; membrane.  
 SEQUENCE 366 AA; 40965 MW; CRC64;  
 42D959BDB8C92C01 CRC64;

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EMBL; AF179666; AAFT6368.1; -
EMBL; AF163365; AAFT2264.1; -
EMBL; LA7334; AAL34349.1; -
HSSP; P30685; 1A9E.
InterPro; IPR007110; Ig-like.
InterPro; IPR0031597; Ig CL.
InterPro; IPR0031596; Ig_NHC.
InterPro; IPR001039; MHC_I.
Pfam; PF00047; Ig; 1.
Pfam; PF00129; MHC_I; 1.
PRINTS; PR01638; MHCCASSI.
ProDom; PD000050; MHC_I; 1.
SMART; SM00407; IgCL1; 1.
PROSITE; PS550835; Ig_LIKE; 1.
Glycoprotein; MHC; Transmembrane.
SEQUENCE 366 AA; 40965 MW; D96A1B4870D489F4 CRC64;

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RESULT 43						
Q8CWZ7	Q8CWZ7	PRELIMINARY;	PRT;	449	AA.	
ID	Q8CWZ7					
AC	Q8CWZ7;					
DT	01-MAR-2003	(TRIMBLrel.	23,	Created)		
DT	01-MAR-2003	(TRIMBLrel.	23,	Last sequence update)		
DT	01-MAR-2003	(TRIMBLrel.	23,	Last annotation update)		
DE	Putative carbon efflux pump (Multi-drug resistance protein).					
Qy	249	VIVVLAVAL	256			
Db	317	VIVVLAVAL	324			
Query Match	2.65;	Score	8;	DB	7;	Length 366;
Best Local Similarity	100.0%	Pred.	No.	17;		
Matches	8;	Mismatches	0;	Indels	0;	Gaps
Conservative						

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Query Match Similarity 2.63%; Score 8; DB 17; Length 366;
Best Local Similarity 100.0%; Pred. NO. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GN OS Streptococcus mutans  
OC Bacteria; Firmicutes  
OC Streptococcus.

249 VLVVVLAVL 256  
317 VLVVVLAVL 324

NCBI\_FAXID=1309;  
[1]  
RN  
RP  
SEQUENCE FROM N.A

Query Match	Similarity
Best Local Matches	Consimilarity
EMBL; AE014859; ADR	8:
Complete proteome	9:
SEQUENCE 449 AA	9:
SQ	9:

RECORDS 100  
MEDLINE=22395063;  
Ajdic D., McSweeney RA, Carson M.B., Print RA, Li S., Zhu H., Naam, "Genome sequence pathogen," Proc. Natl. Acad. Sci. USA, 95, 14785-14790, 1998, R1-R7, R11-R12, DR, KW, SEQUENCE 449 AA



RT	lactis ssp. lactis II1403;"	Query	Match 2.6%; Score 8; DB 13;
DR	Genome Res. 11:1731-73 (2001).	Best	Local Similarity 100.0%; Pred. No. 56;
EMBL	AE005277; AAK0507.1; -.	Matches 8;	Mismatches 0;
DR	InterPro; IPR003706; CstA.	Conservative 0;	Indels 0;
DR	Pfam; PF0554; CstA.	Gaps 0;	Gaps 0;
KW	Complete proteome.		
SEQUENCE	784 AA; 85323 MW;	112 LYRCVVA 119	
SEQUENCE	784 AA; 38F7B2251765158C CRC64;	137 LYRCVVA 144	
Query Match	2.6%; Score 8; DB 16; Length 784;	RESULT 49	
Best Local Similarity 100.0%; Pred. No. 35;	Matches 8;	Q8N185	PRELIMINARY;
Conservative 0;	Mismatches 0;	ID	Q8N185;
Indels 0;	Gaps 0;	AC	Q8N185;
Db	252 VLAVALI 259	DT	01-OCT-2002 (TREMBUREL. 22, Created)
Db	223 VLAVALI 230	DT	01-OCT-2002 (TREMBUREL. 22, Last sequence update)
Db	23 VLAVALI 230	DT	01-OCT-2002 (TREMBUREL. 22, Last annotation update)
RESULT 48		DE	OK/SW-CL. 4.
Q9W6E1	PRELIMINARY;	GN	OK/SW-CL. 4.
ID	Q9W6E1;	OS	Homo sapiens (Human).
AC	Q9W6E1;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DT	01-NOV-1999 (TREMBUREL. 12, Created)	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
DT	01-NOV-1999 (TREMBUREL. 12, Last sequence update)	RN	[1]
DT	01-MAR-2003 (TREMBUREL. 23, Last annotation update)	RP	SEQUENCE FROM N.A.
DE	Neurocan core protein.	RA	Shichijo S., Itoh K.
OS	Gallus Gallus (Chicken).	RT	"Identification of immuno-peptidomics that recognized by tumor-reactive
OS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	RT	CTL generated from TIL of colon cancer patients";
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	RT	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
OC	NCBI_TaxID=9031;	RL	DR EMBL: AB062435; BA893498.1; -.
RN	RN	SQ	SEQUENCE 67 AA; 7517 MW; 3BCD63D8E72609C6 CRC64;
RP	SEQUENCE FROM N.A.	RESULT 50	
RX	MEDLINE=200983; PubMed=10851024;	Q99GX8	PRELIMINARY;
RA	Li H., Leung T.C., Hoffman S., Balsamo J., Lillian J.;	ID	Q99GX8;
RT	"Coordinate Regulation of Cadherin and Integrin Function by the	AC	Q99GX8;
RT	Chondroitin Sulfate Proteoglycan Neurocan.";	DT	01-JUN-2001 (TREMBUREL. 17, Created)
RT	J Cell Biol. 149:1275-1288 (2000).	DT	01-JUN-2001 (TREMBUREL. 17, Last sequence update)
RL	DR EMBL: AF116856; AAD24546.2; -.	DT	01-OCT-2002 (TREMBUREL. 22, Last annotation update)
DR	DR HSSP; P08709; 1BF9.	DE	ORF72 (Hypothetical 10.0 kDa protein).
DR	DR InterPro; IPR000152; Asx hydroxyl.	OS	Helicoverpa zea single nucleocapsid nucleopolyhedrovirus,
DR	DR InterPro; IPR000742; EGF_.	OS	Helicoverpa armigera nucleopolyhedrovirus G4, and
DR	DR InterPro; IPR001881; EGF_Ca.	OS	Helicoverpa armigera nuclear polyhedrosis virus.
DR	DR InterPro; IPR001438; EGF_IT.	OC	Viruses; dsDNA viruses, no RNA stage; Baculoviridae.
DR	DR InterPro; IPR005209; EGF_Like.	OC	Nucleopolyhedrovirus.
DR	DR InterPro; IPR003599; Ig.	NCBI_TaxID=10468; 148363; 51313;	[1]
DR	DR InterPro; IPR007110; Ig-like.	RN	SEQUENCE FROM N.A.
DR	DR InterPro; IPR003006; Ig_MHC.	RP	SPECIES=Helicoverpa zea single nucleocapsid nucleopolyhedrovirus;
DR	DR InterPro; IPR001304; lectin_C.	RC	Chen X., Zhang W.J., Wong J., Chun G., Lu A., McCutchan B.F.,
DR	DR InterPro; IPR000538; Link.	RA	Presnall J.K., Hermann R., Dolan M., Tingey S., Hu Z.-H., Viak J.M.;
DR	DR InterPro; IPR000436; Sushi_SCR_CCP.	RT	"Sequence analysis of the gp37 gene of Helicoverpa zea single nucleocapsid nucleopolyhedrovirus.";
PFam	PF00008; EGF; 2.	RT	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
PFam	PF00047; Ig; 1.	RL	[2]
PFam	PF00059; lectin_C; 1.	RN	SEQUENCE FROM N.A.
PFam	PF00084; sushi; 1.	RP	SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;
PFam	PF00193; Xlink; 2.	RC	Chen X., Zhang W.J., Wong J., Chun G., Lu A., McCutchan B.F.,
PRINTS	PRINTS; P00008; EGF_BLOOD.	RA	Deng F., Chen X., Vlak J.M., Arif B.M., Hu Z.-H., Viak J.M.;
DR	DR PROSITE; P00010; Xlink; 2.	RT	"Sequence analysis of the gp37 gene of Helicoverpa zea single nucleocapsid nucleopolyhedrovirus";
DR	DR PROSITE; P000918; Xlink; 2.	RT	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR	DR PROSITE; P000615; C_TYPE_LECTIN_1; 1.	RL	[2]
DR	DR PROSITE; P00041; C_TYPE_LECTIN_2; 1.	RN	SEQUENCE FROM N.A.
DR	DR PROSITE; P00022;	RP	SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;
DR	DR PROSITE; P001186; EGF; 1.	RC	Chen X., Zhang W.J., Wong J., Chun G., Lu A., McCutchan B.F.,
DR	DR PROSITE; P001187; EGF_2; 1.	RA	Deng F., Chen X., Vlak J.M., Arif B.M., Hu Z.-H., Viak J.M.;
DR	DR PROSITE; P001188; EGF_Ca; 1.	RT	"Sequence analysis of the gp37 gene of Helicoverpa zea single nucleocapsid nucleopolyhedrovirus";
DR	DR PROSITE; P001241; Xlink; 2.	RT	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
KW	EGR-1-like domain.	RL	[3]
SEQUENCE	1290 AA; 138877 MW;	RN	SEQUENCE FROM N.A.
SEQUENCE	1290 AA; 182BD86D0E40BE78 CRC64;	RP	SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;

RA Wang H., Hu Z., Sun X., Vlak J.M., Chen X.;  
 RT Sequence analysis of the *lap3* gene of *Heliothis armigera* single-  
 RL nucleocapsid nucleopolyhedrovirus.;  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;  
 RX MEDLINE=210730; PubMed=11210934;  
 RA Wang H., Chen X., Wang H., Arif B.M., Vlak J.M., Hu Z.;  
 RT "Nucleotide sequence and transcriptional analysis of a putative basic  
 DNA-binding protein of *Helicoverpa armigera* polyhedrovirus.;"  
 RL Virus Genes 22:113-120 (2001).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;  
 RX MEDLINE=21064569; PubMed=1125177;  
 RA Chen X., IJkel W.F., Tarchini R., Sun X., Sandbrink H., Wang H.,  
 RA Peters S., Zuidema D., Tarchini R., Sun X., Sandbrink H., Wang H.,  
 RA Peters S., Zuidema D., Lankhorst R.K., Vlak J.M., Hu Z.;  
 RT "The sequence of the *Helicoverpa armigera* single-nucleocapsid  
 nucleopolyhedrovirus genome.";  
 RL J. Gen. Virol. 82:241-257(2001).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;  
 RA Chen X., IJkel W.F., Tarchini R., Sun X., Sandbrink H., Wang H.,  
 RA Peters S., Zuidema D., Lankhorst R.K., Vlak J.M., Hu Z.;  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Helicoverpa armigera nuclear polyhedrosis virus; STRAIN=C1;  
 RX PubMed=12050807;  
 RA Zhang C.X., Wu J.C.;  
 RT "Genome structure and the p10 gene of the *Helicoverpa armigera*  
 nucleopolyhedrovirus.";  
 RL Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 33:179-184 (2001).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Helicoverpa armigera nuclear polyhedrosis virus; STRAIN=C1;  
 RA Zhang C.X., Jin W.R.;  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF334030; AAL56078.1; -;  
 DR EMBL; AF271059; AAG53813.1; -;  
 DR EMBL; AF301045; AAK98317.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 85 AA; 9958 MN; 6560D8FAA06A6787 CRC64;  
 Query Match 2.3%; Score 7; DB 12; Length 85;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 18 FFULLLF 24  
 Db 28 FFULLLF 34

Search completed: December 15, 2003, 15:00:24  
 Job time : 46 secs

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